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RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/741,843

TIME: 15:31:38

Input Set : A:\MS.txt

Output Set: N:\CRF3\10292001\I741843.raw

3 <110> APPLICANT: LEUNG, Shui-on
 4 HANSEN, Hans
 6 <120> TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA

7 AND LEUKEMIA CELLS

9 <130> FILE REFERENCE: 018733/0996

11 <140> CURRENT APPLICATION NUMBER: US 09/741,843

12 <141> CURRENT FILING DATE: 2000-12-22

14 <150> PRIOR APPLICATION NUMBER: US 09/127,902

15 <151> PRIOR FILING DATE: 1998-08-03

17 <150> PRIOR APPLICATION NUMBER: US 08/690,102

18 <151> PRIOR FILING DATE: 1996-07-06

20 <150> PRIOR APPLICATION NUMBER: US 08/289,576

21 <151> PRIOR FILING DATE: 1994-08-12

23 <160> NUMBER OF SEQ ID NOS: 21

25 <170> SOFTWARE: PatentIn version 3.1

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 339

29 <212> TYPE: DNA

30 <213> ORGANISM: Murinae gen. sp.

32 <220> FEATURE:

33 <221> NAME/KEY: CDS

34 <222> LOCATION: (1)..(339)

35 <223> OTHER INFORMATION:

38 <400> SEQUENCE: 1

39 gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga 48
 40 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 41 1 5 10 15
 43 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
 44 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 45 20 25 30
 47 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
 48 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 49 35 40 45
 51 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
 52 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 53 50 55 60
 55 cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
 56 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 57 65 70 75 80
 59 atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
 60 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
 61 85 90 95
 63 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336
 64 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 65 100 105 110
 67 cgt 339
 68 Arg

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 75 <213> ORGANISM: Murinae gen. sp.
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 80 1 5 10 15
 83 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 84 20 25 30
 87 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 88 35 40 45
 91 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 92 50 55 60
 95 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 96 65 70 75 80
 99 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
 100 85 90 95
 103 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 104 100 105 110
 107 Arg

111 <210> SEQ ID NO: 3
 112 <211> LENGTH: 348
 113 <212> TYPE: DNA
 114 <213> ORGANISM: Murinae gen. sp.
 116 <220> FEATURE:
 117 <221> NAME/KEY: CDS
 118 <222> LOCATION: (1)..(348)
 119 <223> OTHER INFORMATION:

122 <400> SEQUENCE: 3
 123 cag gtc cag ctg cag gag tca ggg gct gaa ctg tca aaa cct ggg gcc 48
 124 Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
 125 1 5 10 15
 127 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
 128 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 129 20 25 30
 131 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144
 132 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 133 35 40 45
 135 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
 136 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
 137 50 55 60
 139 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240
 140 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 141 65 70 75 80
 143 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
 144 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 145 85 90 95
 147 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336
 148 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu

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157 <211> LENGTH: 116
158 <212> TYPE: PRT
159 <213> ORGANISM: Murinae gen. sp.
161 <400> SEQUENCE: 4
163 Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
164 1          5          10          15
167 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
168          20          25          30
171 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
172          35          40          45
175 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
176          50          55          60
179 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
180 65          70          75          80
183 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
184          85          90          95
187 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
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191 Thr Val Ser Ser
192          115
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 339
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(339)
203 <223> OTHER INFORMATION:
206 <400> SEQUENCE: 5
207 gac att cag ctg acc cag tct cca tca tct ctg agc gca tct gtt gga
208 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
209 1          5          10          15
211 gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt
212 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
213          20          25          30
215 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa
216 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
217          35          40          45
219 gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc
220 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
221          50          55          60
223 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc
224 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
225 65          70          75          80

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227 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa      288
228 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
229           85                      90                      95
231 tac ctc tcc tcc tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa      336
232 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
233           100                      105                      110
235 cgt      339
236 Arg
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 113
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 6
247 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
248 1           5                      10                      15
251 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
252           20                      25                      30
255 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
256           35                      40                      45
259 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
260           50                      55                      60
263 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
264 65           70                      75                      80
267 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
268           85                      90                      95
271 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
272           100                      105                      110
275 Arg
279 <210> SEQ ID NO: 7
280 <211> LENGTH: 348
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: CDS
286 <222> LOCATION: (1)..(348)
287 <223> OTHER INFORMATION:
290 <400> SEQUENCE: 7
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292 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
293 1           5                      10                      15
295 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
296 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
297           20                      25                      30
299 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att      144
300 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
301           35                      40                      45
303 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
304 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
305           50                      55                      60

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307 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac      240
308 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
309 65                               70                               75                               80
311 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt      288
312 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
313                               85                               90                               95
315 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc      336
316 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
317                               100                            105                            110
319 acc gtc tcc tcg                                                    348
320 Thr Val Ser Ser
321      115
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 116
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 8
331 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
332 1                               5                               10                               15
335 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
336      20                               25                               30
339 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
340      35                               40                               45
343 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
344      50                               55                               60
347 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
348 65                               70                               75                               80
351 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
352      85                               90                               95
355 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
356      100                            105                            110
359 Thr Val Ser Ser
360      115
363 <210> SEQ ID NO: 9
364 <211> LENGTH: 116
365 <212> TYPE: PRT
366 <213> ORGANISM: Homo sapiens
368 <400> SEQUENCE: 9
370 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
371 1                               5                               10                               15
374 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
375      20                               25                               30
378 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
379      35                               40                               45
382 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
383      50                               55                               60
386 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
387 65                               70                               75                               80
390 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys

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VERIFICATION SUMMARY

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